METALEPTEA
THE NEWSLETTER OF THE ORTHOPTERISTS' SOCIETY

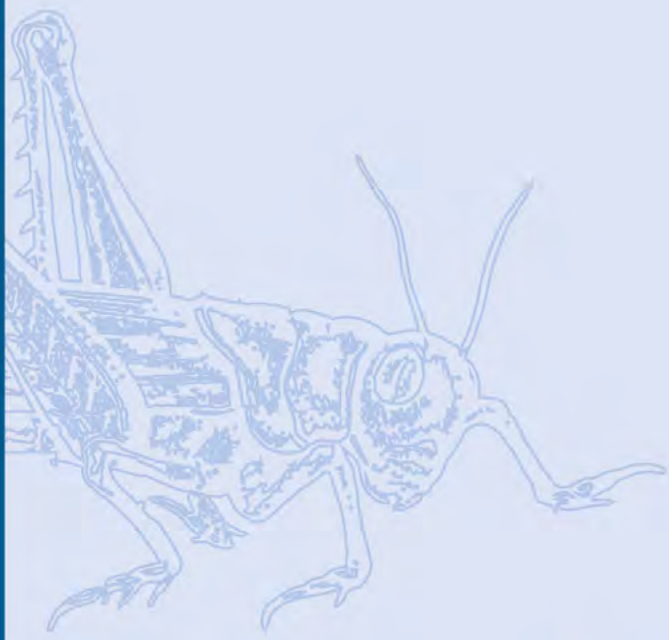
13TH INTERNATIONAL CONGRESS OF ORTHOPTEROLOGY

13TH INTERNATIONAL CONGRESS OF ORTHOPTEROLOGY

ABSTRACT BOOK 2019

AGADIR,
MOROCCO
24 - 28 MARCH2019

www.ico2019morocco.com



CONGRESS SECRETARIAT

Sciences Faculty, University Ibn Zohr
AGADIR | MOROCCO
orthoptera2019@uiz.ac.ma

Design & Print PIXEL CONCEPT.MA

www.ico2019morocco.com

Population and landscape genomics of Orthopterans

INTEGRATIVE SYSTEMATIC REVISION REVEALS CRYPTIC SPECIES IN THE CALLIPTAMUS GENUS

Marie-Pierre Chapuis[1], Laure Benoit[1], Antoine Foucart[1], Alexandre Dehne Garcia[2], Jean-Yves Rasplus[2], Nicolas Leménager[1], Bruno Michel[1], Armelle Coeur d'Acier[2]

[1] Centre de coopération internationale en recherche agronomique pour le développement (CIRAD), UMR Centre de Biologie pour la Gestion des Populations (CBGP), CS 30016, Montferrier-sur-Lez, France; marie-pierre.chapuis@cirad.fr

[2] INRA, UMR CBGP, F-34398 Montpellier, France

The systematics of the genus *Calliptamus* mainly relies on the shape of the wing and phallic complex, and on color pattern of hind femora of males only. However, geographical variation in these morphological characters hinders species determination. These difficulties may explain why the species delimitation within the genus *Calliptamus* has been controversial, with numerous confusions, descriptions, synonymies and subspecies. The purpose of this research is to provide a taxonomic review of the genus *Calliptamus*, based on an integrative approach including morphological, molecular and biological data. Beyond laying the foundations for a revised classification, this project will unravel the historical biogeography of the genus.

The Orthoptera Species File currently counts twelve species whose type depositories are known for the Palaearctic genus *Calliptamus*. We collected with success 9 species, represented by an average of 10 (from 1 to 25) individuals and 6 (from 1 to 17) localities. Since a phylogeny based on a few nuclear genes only may fail to resolve the basal relationships, we used the method of Restriction-site-associated DNA sequencing (RAD-seq), which showed promises to infer shallow relationships in insects. We showed a success of the method, despite the huge size for the genomes of Calliptamus sp., which we estimated to be ~7.65-8.39 Gb. We confirmed the two clades defined on the basis of genitalia shape: a Northern group includes species from the cold and wet temperate regions of Eurasia (e.g. *C. italicus*) and a southern group includes species from the warm and dry mediterranean region (e.g. *c. barbarus*). we interpreted diversification within these two clades as the result of biogeographic factors, such as isolation in high mountain ranges and islands. We discovered that the species *C. barbarus* was not monophyletic and we used finer-scale sampling and the COI barcode to understand further its evolutionary history. Morphological analyses of numerous characters, including the hind wing, hind femur, shape of the pronotum and internal and external structures of the male genitalia, are in process to supplement genetic analyses.

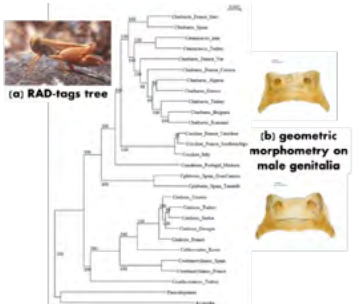


Figure 1. Phylogenetic tree inferred from RADseq data for 26 *Calliptamus* individuals and 2 outgroup taxa using RADIS (a) and Illustration of geometric morphometry on male genitalia of *C. barbarus* and *C. italicus*.

Key Words: *Calliptamus*, RAD-Seq, morphology, cryptic species, haplotype network, glaciation.